

us-09-195-368-1-1.rag

Fri Feb 23 10:49:07 2001

Ashkenazi AJ, Baker KP, Godowski PJ, Gurney AL;
Mark MR, Marsters SA, Pitti R;
WPI; 1999-338009/28.
N-PSDB; X59744.

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(GETH) GENENTECH INC.

Ashkenazi AJ, Goddard A, Gurney AL, Marsters SA;
Pitti RM, Wood WI;
WPI; 1999-494296/41.
N-PSDB; X87726.

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Tumour necrosis factor receptor homologue - useful for, e.g.
modulating apoptosis and NF-KB activation and proinflammatory or
autoimmune responses

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Example 2; Fig 5A; 104pp; English.

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The present sequence represents a putative ligand for PRO364 (see
also Y06605), a novel member of the tumour necrosis factor
receptor family. The sequence was deduced from an isolated cDNA
clone (see X87726). Hydropathy analysis suggests a type II
transmembrane homology. The mol.wt. is 20,308. Identity is
shown to human Apo-2L (19.8%), Fas/Apo-1-ligand (19.0%), TNF-alpha
(20.6%) and lymphotokine-alpha (17.5%). PRO364 is useful for
modulating apoptosis, NF-KB activation and proinflammatory or
autoimmune responses in mammalian cells.

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Query Match 100.0%; Score 951; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 100.0%; Score 951; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 100.0%; Score 951; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 100.0%; Score 951; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 100.0%; Score 951; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 100.0%; Score 951; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 100.0%; Score 951; DB 20; Length 177;
Best Local Similarity 100.0%; Pred. No. 6,5e-98;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
 KW Immunomodulation; inflammation; cell proliferation; angiogenesis;
 KW tumour metastasis; apoptosis; sepsis; endotoxemia.
 XX Homo sapiens.
 XX US5998171-A.
 XX 07-DEC-1999.
 XX 15-AUG-1997; 97US-0912227.
 XX 16-AUG-1996; 96US-0024058.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ni J, Rosen CA, Yu G;
 XX WPI: 1998-169182/15.
 XX N-PSDB; V19195.
 XX Nucleic acid encoding human endokine-alpha - useful for diagnosis
 XX and treatment of tumour necrosis factor-related diseases
 XX Claim 1; Fig 1A-B; 78pp; English.
 XX This polypeptide comprises human endokine-alpha, a novel member of
 XX the tumour necrosis factor (TNF) family of cytokines that shows
 XX 30% similarity and 22% identity to human TNF-alpha. Its amino
 XX acid sequence was deduced from a human striatum cDNA clone (see
 XX V19195). Isolation of this nucleic acid allows production of
 XX recombinant endokine-alpha polypeptides in transformed host cells.
 XX Endokine-alpha may be involved in disorders of immunomodulation,
 XX infection, cell proliferation, angiogenesis, tumour metastasis,
 XX apoptosis, sepsis and endotoxaemia, and may be useful for treating
 XX melanoma and sarcoma, particularly where coupled to a radioisotope
 XX or cytostatic agent. Antibodies raised against endokine-alpha are
 XX useful diagnostically and for treatment of TNF-associated disease.
 XX Sequence 169 AA;
 SQ
 Query Match 95.3%; Score 906; DB 19; Length 169;
 Best Local Similarity 100.0%; Pred. No. 6.1e-93;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 MPLSHRTGAGRSWKWLFLCSFVLMFLFCSFSLIFLQLETAKEPCMAKFGPLPSK 68
 Db 1 mplshrtgagrswwkwlflcsfsvlmflfcsfswlflqltaketakepcmakfgplpsk 60
 QY 69 WQMASSEPCVKNKVSQWKLLEILQNGLYLYIGQVAPNANYNDVAPFEVRLYKKNKDMTQTLT 128
 Db 61 wqmassepcvknkvsdwkllqnglylyigqvapnanyndvapevrllyknkdmqtlit 120
 QY 129 NKSQIQNVGTYELHVGDTIDLFNSEHQVLKNTYWGIIILLANPQFIS 177
 Db 121 nkskinqvgtyelhvgdtidlfnsqhqlvknntywgiiillanpqfils 169
 RESULT 5
 ID P60547 standard; Protein: 326 AA.
 XX AC P60547;
 XX 24-JUN-1991 (first entry)
 XX Segment 8 clone of the hu/5 rotavirus.
 XX Hu/Australia/5/77 rotavirus; vaccine.
 XX Human/5 rotavirus.
 XX WO8505122-A.
 XX 21-NOV-1985.
 XX 29-APR-1985; 85WO-AU00096.
 PF

XX Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
 KW Immunomodulation; inflammation; cell proliferation; angiogenesis;
 KW tumour metastasis; apoptosis; sepsis; endotoxemia.
 XX Homo sapiens.
 XX US5998171-A.
 XX 07-DEC-1999.
 XX 15-AUG-1997; 97US-0912227.
 XX 16-AUG-1996; 96US-0024058.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ni J, Rosen CA, Yu G;
 XX WPI: 2000-1104608/09.
 XX N-PSDB; Z57314.
 XX Isolated human endokine alpha gene useful as a diagnostic probes and
 XX primers
 XX Claim 1; Fig 1; 31pp; English.
 XX The present sequence represents human endokine alpha which is a member
 XX of the tumour necrosis factor (TNF) family of cytokines. Endokine alpha
 XX protein and polynucleotides can be used in diagnostic and therapeutic
 XX methods concerning TNF family-related disorders. These include disorders
 XX associated with immunomodulation and inflammation, cell proliferation,
 XX angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxemia.
 XX Sequence 169 AA;
 SQ
 Query Match 95.3%; Score 906; DB 21; Length 169;
 Best Local Similarity 100.0%; Pred. No. 6.1e-93;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 MPLSHRTGAGRSWKWLFLCSFVLMFLFCSFSLIFLQLETAKEPCMAKFGPLPSK 68
 Db 1 mplshrtgagrswwkwlflcsfsvlmflfcsfswlflqltaketakepcmakfgplpsk 60
 QY 69 WQMASSEPCVKNKVSQWKLLEILQNGLYLYIGQVAPNANYNDVAPFEVRLYKKNKDMTQTLT 128
 Db 61 wqmassepcvknkvsdwkllqnglylyigqvapnanyndvapevrllyknkdmqtlit 120
 QY 129 NKSQIQNVGTYELHVGDTIDLFNSEHQVLKNTYWGIIILLANPQFIS 177
 Db 121 nkskinqvgtyelhvgdtidlfnsqhqlvknntywgiiillanpqfils 169
 RESULT 5
 ID P60547 standard; Protein: 326 AA.
 XX AC P60547;
 XX 24-JUN-1991 (first entry)
 XX Segment 8 clone of the hu/5 rotavirus.
 XX Hu/Australia/5/77 rotavirus; vaccine.
 XX Human/5 rotavirus.
 XX WO8505122-A.
 XX 21-NOV-1985.
 XX 29-APR-1985; 85WO-AU00096.
 PF

RESULT	6	
WI0344		
ID	WI0344	standard; Protein; 2763 AA.
XX	AC	WI0344;
XX	XX	
DT	15-APR-1997	(first entry)
XX	XX	Maize dwarf mosaic virus polyprotein.
DE	XX	MDMV-B; viral resistance; disease resistance; transgenic plant;
XX	XX	monocot; P3 proteinase; N1A proteinase; N1B replicase;
KW	KW	RNA-dependent RNA polymerase; Coat protein; Zea mays; sorghum;
KW	KW	sugarcane; Saccharum officinale.
OS	XX	Maize dwarf mosaic virus strain B.
XX	XX	
Key		Location/Qualifiers
FT	Protein	1..377
FT	FT	/label= HC-Pro
FT	FT	/note= "portion of the helper component-P2 proteinase"
FT	FT	263..336
FT	Domain	/note= "MDMV-B HC-Pro domain"
FT	FT	378..791
FT	Protein	

FT		/label= p3_proteinase	
FT	Protein	/note= "claimed polypeptide (Claim 20)"	
FT		792..1430	
FT		/label= "Cylindrical_inclusion_protein	
FT	Domain	/note= "claimed polypeptide (Claim 20)"	
FT		880..1010	
FT	Protein	/note= "conserved helicase domain"	
FT		1431..1483	
FT		/label= K2	
FT	Protein	/note= "6 kDa protein"	
FT		1484..1914	
FT		/label= N1a_proteinase	
FT	Protein	/note= "claimed polypeptide (Claim 20)"	
FT		1915..2435	
FT		/label= N1b_replicase	
FT	Region	/note= "claimed polypeptide (Claim 20)"	
FT		2266..2268	
FT		/note= "conserved motif characteristic of	
FT	Protein	RNA-dependent replicases"	
FT		2436..2763	
FT	Misc-difference	/label= Coat_protein	
FT		144	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		704	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		712	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		829	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		834	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		843	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		847	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		852	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		1346	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		1362	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		2077	
FT	Misc-difference	/note= "unidentified amino acid"	
FT		2385	
FT	Misc-difference	/note= "unidentified amino acid"	
XX			
PN	WO9702352-A1.		
XX			
PD	23-JAN-1997.		
XX			
PE	20-JUN-1996; 96WO-EP02673.		
XX			
PR	30-JUN-1995; 95US-0496944.		
XX			
PA	(CIBA) CIBA GEIGY AG.		
XX			
PJ	Dietz JM, Law MD;		
XX			
DR	WPI; 1997-108965/10.		
DR	N-PSDB; T47073.		
XX			
PT	Chimaeric gene for imparting viral resistance to plants - contains		
PT	sequence modified to express non-translatable mRNA, or non-coat		
PT	viral protein		
XX			
XX	Claim 20; Page 31-44; 64pp; English.		
PS			
XX			
CC	The sequence of the polyprotein encoded by the polycistronic mRNA		
CC	(T47073) of maize dwarf mosaic virus strain B (MDMV-B) is given in		
CC	w10344. New chimaeric genes comprise a monocotyledonous plant		
CC	promoter linked to a modified nucleic acid sequence derived from		
CC	the MDMV-B genome. The modification is such that mRNA is translated		
CC	to a truncated protein (pref. smaller than 200 amino acids), no		

CC Note: This sequence does not appear in the specification. It has
 XX been created from the parent CAP-1 sequence provided in Fig 1.
 SQ Sequence 472 AA;

Query Match 7.8%; Score 74.5; DB 17; Length 472;
 Best Local Similarity 25.5%; Pred. No. 5.6;
 Matches 36; Conservative 20; Mismatches 42; Indels 43; Gaps 8;
 QY 30 CSIVMLLFCFSWLFIFLOLETAKEPCMAKFGPLPSKQWMASSPPPCVKNVSDW---- 85
 Db 128 cvvscphkcsvqtl-----lrsegtnqika-----heassavghvnlkewsnsl 174
 QY 86 --KLEILQGLYLIYGOVAPNAN----YNDVAPFEVRLYKKNKDMIQTLNKSQKIONVGGT 139
 Db 175 ekvsvllqn-----esveknksiqslhngicsfeieierqkemir--nneski----- 220
 QY 140 YELHVGDTIDLFNSEQHVLK 160
 Db 221 --lhqrvld-----sqaeklk 235

RESULT 9
 R98833
 ID R98833 standard; Protein; 543 AA.
 AC R98833;
 DT 23-MAR-1998 (first entry)
 DE CD40 associated protein (CAP)-1.
 KW CD40 associated protein; CAP; agonist; antagonist; gene therapy;
 KW cell proliferation; treatment; cancer; autoimmune disease.
 OS Homo sapiens.

Key Location/Qualifiers
 Domain 53..91
 FT /note= "RING finger domain"
 FT 117..141
 FT /note= "zinc finger domain 1"
 FT 148..170
 FT /note= "zinc finger domain 2"
 FT 177..197
 FT /note= "zinc finger domain 3"
 FT 384..540
 FT /note= "TRAF domain"
 PN WO9616665-AL.
 XX
 PD 06-JUN-1996.
 XX
 PF 04-DEC-1995; 95WO-US15695.
 XX
 PR 02-DEC-1994; 94US-0349357.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Reed JC, Sato T;
 XX
 DR WPI; 1996-286818/29.
 DR N-PSDB; T30773.
 XX
 PT New CD40 associated protein, agonists and antagonists - used to
 PT modulate cell proliferation, immune response, apoptosis etc., e.g.
 PT for treating cancer or autoimmune disease
 PS Claim 3; Fig 1; 94pp; English.
 XX
 CC This is a CD40 associated protein (CAP)-1. This CAP is a protein that
 CC specifically binds to CD40, a cell surface receptor involved in

CC apoptosis. Agonists and antagonists of CAP can increase or decrease
 CC the level of CAP expression in a cell and can thereby modulate the
 CC function of the cell. Such compounds can be used to treat cancer,
 CC autoimmune diseases like asthma, hay fever, rheumatoid arthritis and
 CC immunodeficiency diseases and neurodegeneration. Antibodies that bind
 CC specifically to CAP can be used to assay CAP, to detect pathologically
 CC altered levels. The encoding nucleic acid can be used to identify
 XX related genes and to express CAP for gene therapy.

SQ Sequence 543 AA;

Query Match 7.8%; Score 74.5; DB 17; Length 543;
 Best Local Similarity 25.5%; Pred. No. 6.8;
 Matches 36; Conservative 20; Mismatches 42; Indels 43; Gaps 8;
 QY 30 CSIVMLLFCFSWLFIFLOLETAKEPCMAKFGPLPSKQWMASSPPPCVKNVSDW---- 85
 Db 199 cvvscphkcsvqtl-----lrsegtnqika-----heassavghvnlkewsnsl 245
 QY 86 --KLEILQGLYLIYGOVAPNAN----YNDVAPFEVRLYKKNKDMIQTLNKSQKIONVGGT 139
 Db 246 ekvsvllqn-----esveknksiqslhngicsfeieierqkemir--nneski----- 291
 QY 140 YELHVGDTIDLFNSEQHVLK 160
 Db 292 --lhqrvld-----sqaeklk 306

RESULT 10
 W27432
 ID W27432 standard; Protein; 543 AA.
 AC W27432;
 DT 27-MAR-1998 (first entry)
 DE Human CRAF1 isoform p55del9.
 XX
 KW CD40 receptor associated factor 1; CRAF1-a; TRAF-3; p55; human;
 KW CD40 mediated intracellular signalling; organ rejection; allergy;
 KW hay fever; autoimmune disease; systemic lupus erythematosus;
 KW rheumatoid arthritis; myasthenia gravis; Graves' disease;
 KW idiopathic thrombocytopenia purpura; haemolytic anaemia;
 KW diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
 KW apoptosis; Rieter's syndrome; spondylarthritis; Lyme disease; HIV;
 KW syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;
 KW pneumoconiosis; adult respiratory distress syndrome; pneumonitis;
 KW asbestosis; silicoconiosis; Farmer's lung; hepatitis; cirrhosis;
 KW atherosclerosis; multiple sclerosis; glomerulonephritis;
 KW glomerulosclerosis; glomerulopathy; kidney disease; nephropathy;
 KW endocarditis; leprosy; malaria; Goodpasture's disease;
 KW Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
 KW Wegener's granulomatosis; cryoimmunoglobulinaemia;
 KW Waldenstrom's macroglobulinaemia; amyloidosis; Sjogren's syndrome;
 KW AIDS; oesophageal dysmotility; inflammatory bowel disease;
 KW bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;
 KW Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
 KW gene therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PH
 XX
 Key Location/Qualifiers
 Region 117..141
 FT /note= "zinc finger 1 (zinc binding to Cys-117,
 FT Cys-124, His-136 and Cys-141)"
 FT 148..170
 FT /note= "zinc finger 2 (zinc binding to Cys-148,
 FT Cys-153, His-165 and Cys-170)"
 FT 177..197
 FT /note= "zinc finger 3 (zinc binding to Cys-177,
 FT Cys-180, His-192 and Cys-197)"
 XX

1. Fic 1A-O: 158pp; English.

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CD40 receptor associated factor 1; CRAF1-b; TRAF-3; p70; human;
CD40 mediated intracellular signalling; organ rejection; allergy;

CC system to screen for immunosuppressant drugs.
XX
SQ Sequence 567 AA;

Query Match
Best Local Similarity 7.8%; Score 74; DB 17; Length 567;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;
QY 72 ASSEPPCVNKVSDW-----KLEILONGLYLIYGVAPNAN-----YNDVAPFEVRLYKKNK 121
Db 252 assavghvnlkewsnlslekkvslq-----esveknksigslnhqcfsfeierqk 305
QY 122 DMIOQLTNKSKIQNVGGTYELHVGDTIDLFNSEHVLK 160
Db 306 emlr--nneski-----lhqrvid-----sqaeklk 330

RESULT 15
W03146
ID W03146 standard; Protein; 568 AA.
AC W03146;
XX
DT 23-OCT-1996 (first entry)
XX
DE LMP1 associated protein LMP1.
XX
KW LMP1; LMP1 associated protein 1; latent infection membrane protein;
KW tumour necrosis factor receptor associated factor; TRAF;
KW signal transduction; TNF; TNFR; lymphoblast; tumorigenesis; AIDS;
KW Hodgkin's disease; Burkitt's lymphoma; nasopharyngeal carcinoma;
KW mononucleosis; Epstein-Barr virus; EBV; therapy.
XX
OS Homo sapiens.

Key Location/Qualifiers
FH Domain 245..568
FT Domain /Label= LMP1-Binding_domain
FT Domain 309..341
FT Domain /Label= Coiled_coil_domain
FT Domain 406..568
FT Domain /Label= Carboxy-terminal domain
PN W09620723-A1.
XX
PD 11-JUL-1996.
XX
PF 28-DEC-1995; 95WO-US16980.
XX
PR 30-DEC-1994; 94US-0367540.
XX
PA (BGMH) BRIGHAM & WOMENS HOSPITAL.
PA (REGC) UNIV CALIFORNIA.
XX
PI Birkenbach M, Kaye KM, Kieff E, Mosialos G, Vanarsdale T;
PI Ware C;
XX
WPI: 1996-333765/33.
DR N-PSDB; T31273.
XX

Compounds and methods for controlling TRAF-mediated signals - by
modulating interactions between Epstein Barr virus encoded proteins
LMP1, LMP1, TNF, TNFR to inhibit lymphoblast growth and
tumorigenesis.
XX
PS Claim 74; Page 58-60; 87pp; English.
XX
CC A novel human B-cell protein (W03146), termed LMP1 associated protein
CC 1 or LMP1, strongly associates with the cytoplasmic C-terminal domain
CC (W03148) of Epstein-Barr virus (EBV) latent infection membrane protein
CC 1 (LMP1), a domain that is stringently required for transformed cell
CC growth. LMP1 is related to murine tumour necrosis factor receptor

CC associated factor TRAF2. A related novel B-cell protein (W03147),
CC EBV6, appears to be the human homologue of murine TRAF1. LMP1
CC polypeptides, esp. the LMP1 binding domain, coiled coil domain and
CC C-terminal domain can be used to inhibit LMP1-TRAF interaction.
CC such polypeptides, which may be obtained by recombinant means (see
CC also T31273) can be used to treat infection and control cell growth
CC or tumorigenesis associated with LMP1-encoding viruses, partic. EBV.
XX
SQ Sequence 568 AA;

Query Match
Best Local Similarity 7.8%; Score 74; DB 17; Length 568;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;
QY 72 ASSEPPCVNKVSDW-----KLEILONGLYLIYGVAPNAN-----YNDVAPFEVRLYKKNK 121
Db 253 assavghvnlkewsnlslekkvslq-----esveknksigslnhqcfsfeierqk 306
QY 122 DMIOQLTNKSKIQNVGGTYELHVGDTIDLFNSEHVLK 160
Db 307 emlr--nneski-----lhqrvid-----sqaeklk 331

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Job time: 131 sec